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<110> Better, Marc D.
Horwitz, Arnold H.

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<150> 60/459,334

<151> 2003-03-31

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<170> PatentIn version 3.2

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| Val | Thr | Leu | Gly | Thr | Ser | Gly | Ser | Ile | Ser | Cys | Arg | Ser | Ser | Lys | Ser | |
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| Leu | Leu | His | Ser | Asn | Gly | Ile | Thr | Tyr | Leu | Tyr | Trp | Tyr | Leu | Gln | Lys | |
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| | | | | | | | | | | | | | | | | |
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| Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr | |
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| Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gly Gly Thr Lys | |
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| ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat | 528 |
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| 160 165 170 | |
| agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa | 624 |
| Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys | |
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| gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag | 672 |
| Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln | |
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| ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag | 720 |
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Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
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Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
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Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
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Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gly Gly Thr Lys
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Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
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Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
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Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
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 Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
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 Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
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 Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe

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| Gly | Cys | Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro | Val | Thr | Val | Ser | Trp | | |
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| | | 160 | | | | | 165 | | | | | 170 | | | | | |
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| Gln | Ser | Ser | Gly | Leu | Tyr | Ser | Leu | Ser | Ser | Val | Val | Thr | Val | Pro | Ser | | |
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| Ser | Ser | Leu | Gly | Thr | Gln | Thr | Tyr | Ile | Cys | Asn | Val | Asn | His | Lys | Pro | | |
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| Thr | His | Thr | Cys | Pro | Pro | Cys | Pro | Ala | Pro | Glu | Leu | Leu | Gly | Gly | Pro | | |
| | | | 225 | | | | 230 | | | | | | 235 | | | | |
| tca | gtc | ttc | ctc | ttc | ccc | cca | aaa | ccc | aag | gac | acc | ctc | atg | atc | tcc | | 816 |
| Ser | Val | Phe | Leu | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Thr | Leu | Met | Ile | Ser | | |
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| cgg | acc | cct | gag | gtc | aca | tgc | gtg | gtg | gtg | gac | gtg | agc | cac | gaa | gac | | 864 |
| Arg | Thr | Pro | Glu | Val | Thr | Cys | Val | Val | Val | Asp | Val | Ser | His | Glu | Asp | | |
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| cct | gag | gtc | aag | ttc | aac | tgg | tac | gtg | gac | ggc | gtg | gag | gtg | cat | aat | | 912 |
| Pro | Glu | Val | Lys | Phe | Asn | Trp | Tyr | Val | Asp | Gly | Val | Glu | Val | His | Asn | | |
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| Val | Ser | Val | Leu | Thr | Val | Leu | His | Gln | Asp | Trp | Leu | Asn | Gly | Lys | Glu | | |
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| Tyr | Lys | Cys | Lys | Val | Ser | Asn | Lys | Ala | Leu | Pro | Ala | Pro | Ile | Glu | Lys | | |
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| Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr | |
| 350 355 360 365 | |
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| gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag | 1296 |
| Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys | |
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| agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag | 1344 |
| Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu | |
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| gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt | 1392 |
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Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
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Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
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Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
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Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
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Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
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Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
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Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
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Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
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Val Thr Leu Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
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Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
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tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag 384
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95 100 105

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Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
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<220>
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<400> 7
atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct      48
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20                      -15                      -10                      -5

gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc ctg cca      96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro
-1 1                      5                      10

gtc act cct gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt      144
Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
15                      20                      25

ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa      192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
30                      35                      40

cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc      240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                      50                      55                      60

tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc      288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
65                      70                      75

act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac      336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
80                      85                      90

tgt gct cag aac cta gag ctt cca cgg acg ttc ggt cag ggc acc aag      384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
95                      100                      105

ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg      432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
110                      115                      120

cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg      480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                      130                      135                      140

ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat      528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145                      150                      155

aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac      576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
160                      165                      170

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agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa 624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
175 180 185

gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag 672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
190 195 200

ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag 720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205 210 215

<210> 8
<211> 239
<212> PRT
<213> Homo Sapiens

<400> 8

Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20 -15 -10 -5

Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro
-1 1 5 10

Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
15 20 25

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
30 35 40

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45 50 55 60

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
65 70 75

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
80 85 90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
95 100 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
110 115 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125 130 135 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145 150 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
160 165 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
175 180 185

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
190 195 200

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205 210 215

<210> 9
<211> 88
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> KL1 V Region Oligos Human Engineered ING-1 Light Chain (Kappa
low)

<400> 9
tgtcgacacc atgaggttct ctgctcagct tctggggctg cttgtgctct ggatccctgg 60
atccactgca gacatcgtga tgaccag 88

<210> 10
<211> 85
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> KL2 V Region Oligos Human Engineered ING-1 Light Chain (Kappa
low)

<400> 10
actcttacta gaccggcagg agatggaacc tgactctccc agagtgactg gattggagag 60
tgcagactgg gtcatcacga tgtct 85

<210> 11
<211> 88
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> KL3 V Region Oligos Human Engineered ING-1 Light Chain (Kappa
low)

<400> 11
ctgccggtct agtaagagtc tcctacatag taatggcatc acttatttgt attggtatct 60
gcagaaacca gggcagtctc ctcagctg 88

<210> 12
<211> 86
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> KL4 V Region Oligos Human Engineered ING-1 Light Chain (Kappa
low)

<400> 12
tgtcccagat ccactgctac tgaacctgtc tgggaccctt gaggctctgt tagacatctg 60
atagatgagc agctgaggag actgcc 86

<210> 13
<211> 77
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> KL5 V Region Oligos Human Engineered ING-1 Light Chain (Kappa
low)

<400> 13
agcagtggat ctgggacaga tttcactctc aagatcagca gagtggaggc tgaagatgtg 60

ggagtttatt actgtgc

77

<210> 14
<211> 75
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> KL6 V Region Oligos Human Engineered ING-1 Light Chain (Kappa
low)

<400> 14
tttgatttca agcttggtgc cctgaccgaa cgtccgtgga agctctaggt tctgagcaca 60

gtaataaact cccac 75

<210> 15
<211> 22
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> Low Risk Primers Forward Primer: KF ING-1 Light Chain Oligos

<400> 15
ttatgtcgac accatgaggt tc 22

<210> 16
<211> 21
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> Low risk Primers Reverse Primer: KR ING-1 Light Chain Oligos

<400> 16
tttgatttca agcttggtgc c 21

<210> 17
<211> 85
<212> DNA
<213> Homo Sapiens


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<220>
<221> misc_feature
<223> Moderate Risk Primer: KM2 V Region Oligos Human Engineered ING-1
      Light Chain Oligos (Kappa Moderate)

<400> 17
actcttacta gaccggcagg agatggaacc cggctctcca ggagtgactg gcagggagag      60

tggagactgg gtcacacga tgtct                                           85

<210> 18
<211> 1398
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> Low Risk Human Engineered ING-1 Heavy Chain (HC)

<220>
<221> misc_feature
<223> Variable region of HC is Amino Acids is 1-116

<220>
<221> CDS
<222> (1)..(1395)

<220>
<221> mat_peptide
<222> (58)..()

<400> 18
atg gct tgg gtg tcc acc ttg cta ttc ctg atg gca gct gcc caa agt      48
Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
      -15                      -10                      -5

gcc caa gca cag atc cag ttg gtg cag tct gga cct gag gtg aag aag      96
Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
      -1  1                      5                      10

cct gga gag tcc gtc aag atc tcc tgc aag gct tct gga tat acc ttc      144
Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
      15                      20                      25

aca aaa tat gga atg aac tgg gtg aag cag gct cca gga cag ggt tta      192
Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
      30                      35                      40                      45

aag tgg atg ggc tgg ata aac acc tac act gaa gag cca aca tat ggt      240
Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
      50                      55                      60

```

| | |
|---|-----|
| gat gac ttc aag gga cgg ttt acc ttc acc ttg gac acc tct act agc Asp Asp Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser 65 70 75 | 288 |
| act gcc tat ttg gaa atc tct tct ctc cgg agt gag gac acg gct aca Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr 80 85 90 | 336 |
| tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt caa gga Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly 95 100 105 | 384 |
| acc ttg gtc acc gtc tcc tca gcc agc aca aag ggc cca tcg gtc ttc Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe 110 115 120 125 | 432 |
| ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu 130 135 140 | 480 |
| ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp 145 150 155 | 528 |
| aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu 160 165 170 | 576 |
| cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser 175 180 185 | 624 |
| agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro 190 195 200 205 | 672 |
| agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys 210 215 220 | 720 |
| act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro 225 230 235 | 768 |
| tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser 240 245 250 | 816 |
| cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp 255 260 265 | 864 |
| cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn | 912 |

| 270 | 275 | 280 | 285 | |
|---|-----|-----|-----|------|
| gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg | | | | 960 |
| Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val | | | | |
| | 290 | 295 | 300 | |
| gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag | | | | 1008 |
| Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu | | | | |
| | 305 | 310 | 315 | |
| tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa | | | | 1056 |
| Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys | | | | |
| | 320 | 325 | 330 | |
| acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc | | | | 1104 |
| Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr | | | | |
| | 335 | 340 | 345 | |
| ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc | | | | 1152 |
| Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr | | | | |
| | 350 | 355 | 360 | 365 |
| tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag | | | | 1200 |
| Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu | | | | |
| | 370 | 375 | 380 | |
| agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg | | | | 1248 |
| Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu | | | | |
| | 385 | 390 | 395 | |
| gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag | | | | 1296 |
| Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys | | | | |
| | 400 | 405 | 410 | |
| agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag | | | | 1344 |
| Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu | | | | |
| | 415 | 420 | 425 | |
| gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt | | | | 1392 |
| Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly | | | | |
| | 430 | 435 | 440 | 445 |
| aaa tga | | | | 1398 |
| Lys | | | | |

<210> 19
 <211> 465
 <212> PRT
 <213> Homo Sapiens

<400> 19

Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
 -15 -10 -5

Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
 -1 1 5 10

Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 15 20 25

Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45

Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
 50 55 60

Asp Asp Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser
 65 70 75

Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr
 80 85 90

Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
 95 100 105

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 110 115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 160 165 170

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 175 180 185

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 190 195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
240 245 250

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
255 260 265

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
270 275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
320 325 330

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
335 340 345

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
350 355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
400 405 410

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
415 420 425

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
430 435 440 445

Lys

<210> 20
<211> 1398
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> Low + Moderate Risk Human Engineered ING-1 Heavy Chain (HC)

<220>
<221> CDS
<222> (1)..(1395)

<220>
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Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
-15 -10 -5

gcc caa gca cag atc cag ttg gtg cag tct gga gct gag gtg aag aag 96
Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
-1 1 5 10

cct gga gag tca gtc aag atc tcc tgc aag gct tct gga tat acc ttc 144
Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25

aca aaa tat gga atg aac tgg gtg cga cag gct cca gga caa ggt tta 192
Thr Lys Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30 35 40 45

gag tgg atg ggc tgg ata aac acc tac act gaa gag cca aca tat ggt 240
Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
50 55 60

cag aag ttc cag gga cgg ttt acc ttc acc ttg gac acc tct act agc 288
Gln Lys Phe Gln Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser
65 70 75

| | |
|---|-----|
| act gcc tat ttg gaa atc tct tcg ctc cgg agt gag gac acg gct gtg | 336 |
| Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val | |
| 80 85 90 | |
| tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt caa gga | 384 |
| Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly | |
| 95 100 105 | |
| acc ttg gtc acc gtc tcc tca gcc agc aca aag ggc cca tcg gtc ttc | 432 |
| Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe | |
| 110 115 120 125 | |
| ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg | 480 |
| Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu | |
| 130 135 140 | |
| ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg | 528 |
| Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp | |
| 145 150 155 | |
| aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta | 576 |
| Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu | |
| 160 165 170 | |
| cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc | 624 |
| Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser | |
| 175 180 185 | |
| agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc | 672 |
| Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro | |
| 190 195 200 205 | |
| agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa | 720 |
| Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys | |
| 210 215 220 | |
| act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg | 768 |
| Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro | |
| 225 230 235 | |
| tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc | 816 |
| Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser | |
| 240 245 250 | |
| cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac | 864 |
| Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp | |
| 255 260 265 | |
| cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat | 912 |
| Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn | |
| 270 275 280 285 | |
| gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg | 960 |

| | |
|---|------|
| Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val | |
| 290 295 300 | |
| gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag | 1008 |
| Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu | |
| 305 310 315 | |
| tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa | 1056 |
| Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys | |
| 320 325 330 | |
| acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc | 1104 |
| Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr | |
| 335 340 345 | |
| ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc | 1152 |
| Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr | |
| 350 355 360 365 | |
| tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag | 1200 |
| Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu | |
| 370 375 380 | |
| agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg | 1248 |
| Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu | |
| 385 390 395 | |
| gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag | 1296 |
| Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys | |
| 400 405 410 | |
| agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag | 1344 |
| Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu | |
| 415 420 425 | |
| gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt | 1392 |
| Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly | |
| 430 435 440 445 | |
| aaa tga | 1398 |
| Lys | |

<210> 21
 <211> 465
 <212> PRT
 <213> Homo Sapiens
 <400> 21

| |
|---|
| Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser |
| -15 -10 -5 |

Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 -1 1 5 10

Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 15 20 25

Thr Lys Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45

Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
 50 55 60

Gln Lys Phe Gln Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser
 65 70 75

Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 80 85 90

Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
 95 100 105

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 110 115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 160 165 170

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 175 180 185

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 190 195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys

| | | | | | |
|-------------|-------------------------------------|-----------------------------|-----------------|--|-----|
| | 210 | | 215 | | 220 |
| Thr His Thr | Cys Pro Pro Cys Pro | Ala Pro Glu Leu Leu | Gly Gly Pro | | |
| | 225 | 230 | 235 | | |
| Ser Val Phe | Leu Phe Pro Pro Lys | Pro Lys Asp Thr | Leu Met Ile Ser | | |
| | 240 | 245 | 250 | | |
| Arg Thr Pro | Glu Val Thr Cys Val Val Val | Asp Val Ser His Glu Asp | | | |
| | 255 | 260 | 265 | | |
| Pro Glu Val | Lys Phe Asn Trp Tyr Val | Asp Gly Val Glu Val His Asn | | | |
| 270 | 275 | 280 | 285 | | |
| Ala Lys Thr | Lys Pro Arg Glu Glu Gln Tyr | Asn Ser Thr Tyr Arg Val | | | |
| | 290 | 295 | 300 | | |
| Val Ser Val | Leu Thr Val Leu His Gln Asp Trp | Leu Asn Gly Lys Glu | | | |
| | 305 | 310 | 315 | | |
| Tyr Lys Cys | Lys Val Ser Asn Lys Ala Leu Pro | Ala Pro Ile Glu Lys | | | |
| | 320 | 325 | 330 | | |
| Thr Ile Ser | Lys Ala Lys Gly Gln Pro Arg Glu | Pro Gln Val Tyr Thr | | | |
| | 335 | 340 | 345 | | |
| Leu Pro Pro | Ser Arg Asp Glu Leu Thr Lys | Asn Gln Val Ser Leu Thr | | | |
| 350 | 355 | 360 | 365 | | |
| Cys Leu Val | Lys Gly Phe Tyr Pro Ser Asp | Ile Ala Val Glu Trp Glu | | | |
| | 370 | 375 | 380 | | |
| Ser Asn Gly | Gln Pro Glu Asn Asn Tyr Lys Thr Thr | Pro Pro Val Leu | | | |
| | 385 | 390 | 395 | | |
| Asp Ser Asp | Gly Ser Phe Phe Leu Tyr Ser Lys | Leu Thr Val Asp Lys | | | |
| | 400 | 405 | 410 | | |
| Ser Arg Trp | Gln Gln Gly Asn Val Phe Ser Cys | Ser Val Met His Glu | | | |
| 415 | 420 | 425 | | | |

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
430 435 440 445

Lys

<210> 22
<211> 91
<212> DNA
<213> HomoSapiens

<220>
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<223> GL1 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
(gamma low)

<400> 22
tgtcgacacc atggcttggg tgtccacctt gctattcctg atggcagctg cccaaagtgc 60
ccaagcacag atccagttgg tgcagtctgg a 91

<210> 23
<211> 90
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GL2 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
(gamma low)

<400> 23
atattttgtg aaggatatc cagaagcctt gcaggagatc ttgacggact ctccaggctt 60
cttcacctca ggtccagact gcaccaactg 90

<210> 24
<211> 91
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GL3 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
(gamma low)

<400> 24
tggatatacc ttcacaaaat atggaatgaa ctgggtgaag caggctccag gacagggttt 60
aaagtggatg ggctggataa acacctacac t 91

<210> 25
<211> 90
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GL4 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
(gamma low)

<400> 25
cagtgc tagt agaggtgtcc aaggtgaagg taaaccgtcc cttgaagtca tcaccatattg 60
ttggctcttc agtgtagggtg tttatccagc 90

<210> 26
<211> 90
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GL5 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
(gamma low)

<400> 26
gacacctcta ctagcactgc ctatttggaa atctcttctc tccggagtga ggacacggct 60
acatatttct gtgcaagatt tggctctgct 90

<210> 27
<211> 85
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GL6 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
(gamma low)

<400> 27
gaccgatggg ccctttgtgc tggctgagga gacggtgacc aaggttcctt gaccccagta 60

gtccacagca gagccaaatc ttgca

85

<210> 28
<211> 22
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> Human Engineered ING-1 Heavy Chain Oligos-Low Risk Primers
Forward primer:GF

<400> 28
ttatgtcgac accatggctt gg

22

<210> 29
<211> 17
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> Human Engineered ING-1 Heavy Chain Oligos Low Risk Primers
-Reverse Primer GR

<220>
<221> misc_feature
<223> ING-1 Heavy Chain Oligos Low Risk Primers Reverse Primer GR

<400> 29
gaccgatggg cccttttg

17

<210> 30
<211> 90
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GM2 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
+ Moderate Risk Primers

<400> 30
atatatttgatg aaggtatatc cagaagcctt gcaggagatc ttgactgact ctccaggctt

60

cttcacctca gctccagact gcaccaactg

90

<210> 31
<211> 91
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GM3 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
+ Moderate Risk Primers

<400> 31
tggatatacc ttcacaaaat atggaatgaa ctgggtgcga caggctccag gacaaggttt 60
agagtggatg ggctggataa acacctacac t 91

<210> 32
<211> 90
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GM4 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
+ Moderate Risk Primers

<400> 32
cagtgctagt agaggtgtcc aaggtgaagg taaaccgtcc ctggaacttc tgaccatattg 60
ttggctcttc agtgtaggtg tttatccagc 90

<210> 33
<211> 90
<212> DNA
<213> HomoSapiens

<220>
<221> misc_feature
<223> GM5 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
+ Moderate Risk Primers

<400> 33
gacacctcta ctagcactgc ctatttggaa atctcttcgc tccggagtga ggacacggct 60
gtgtatttct gtgcaagatt tggctctgct 90

<210> 34
<211> 720
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> P1=P Human Engineered (low risk) ING1 light Chain with one moderate risk proline change; proline at position 8 (P1)

<220>

<221> CDS

<222> (1)..(717)

<220>

<221> mat_peptide

<222> (61)..()

<400> 34

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| atg | agg | ttc | tct | gct | cag | ctt | ctg | ggg | ctg | ctt | gtg | ctc | tgg | atc | cct | 48 |
| Met | Arg | Phe | Ser | Ala | Gln | Leu | Leu | Gly | Leu | Leu | Val | Leu | Trp | Ile | Pro | |
| -20 | | | | | -15 | | | | | -10 | | | | | -5 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| gga | tcc | act | gca | gac | atc | gtg | atg | acc | cag | tct | cca | ctc | tcc | aat | cca | 96 |
| Gly | Ser | Thr | Ala | Asp | Ile | Val | Met | Thr | Gln | Ser | Pro | Leu | Ser | Asn | Pro | |
| | | | -1 | 1 | | | | 5 | | | | | 10 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gtc | act | ctg | gga | gag | tca | ggg | tcc | atc | tcc | tgc | cgg | tct | agt | aag | agt | 144 |
| Val | Thr | Leu | Gly | Glu | Ser | Gly | Ser | Ile | Ser | Cys | Arg | Ser | Ser | Lys | Ser | |
| | | 15 | | | | 20 | | | | | | 25 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ctc | cta | cat | agt | aat | ggc | atc | act | tat | ttg | tat | tgg | tat | ctg | cag | aaa | 192 |
| Leu | Leu | His | Ser | Asn | Gly | Ile | Thr | Tyr | Leu | Tyr | Trp | Tyr | Leu | Gln | Lys | |
| | 30 | | | | | 35 | | | | | 40 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cca | ggg | cag | tct | cct | cag | ctg | ctc | atc | tat | cag | atg | tct | aac | aga | gcc | 240 |
| Pro | Gly | Gln | Ser | Pro | Gln | Leu | Leu | Ile | Tyr | Gln | Met | Ser | Asn | Arg | Ala | |
| 45 | | | | | 50 | | | | | 55 | | | | | 60 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tca | ggg | gtc | cca | gac | agg | ttc | agt | agc | agt | gga | tct | ggg | aca | gat | ttc | 288 |
| Ser | Gly | Val | Pro | Asp | Arg | Phe | Ser | Ser | Ser | Gly | Ser | Gly | Thr | Asp | Phe | |
| | | | | 65 | | | | | 70 | | | | | 75 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| act | ctc | aag | atc | agc | aga | gtg | gag | gct | gaa | gat | gtg | gga | gtt | tat | tac | 336 |
| Thr | Leu | Lys | Ile | Ser | Arg | Val | Glu | Ala | Glu | Asp | Val | Gly | Val | Tyr | Tyr | |
| | | 80 | | | | | | 85 | | | | | 90 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tgt | gct | cag | aac | cta | gag | ctt | ccg | cgg | acg | ttc | ggg | cag | ggc | acc | aag | 384 |
| Cys | Ala | Gln | Asn | Leu | Glu | Leu | Pro | Arg | Thr | Phe | Gly | Gln | Gly | Thr | Lys | |
| | | 95 | | | | | 100 | | | | | 105 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ctt | gag | atg | aaa | cga | act | gtg | gct | gca | cca | tct | gtc | ttc | atc | ttc | ccg | 432 |
| Leu | Glu | Met | Lys | Arg | Thr | Val | Ala | Ala | Pro | Ser | Val | Phe | Ile | Phe | Pro | |
| | 110 | | | | | 115 | | | | | 120 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cca | tct | gat | gag | cag | ttg | aaa | tct | gga | act | gcc | tct | gtt | gtg | tgc | ctg | 480 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | |
|--------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Asp | Glu | Gln | Leu | Lys | Ser | Gly | Thr | Ala | Ser | Val | Val | Cys | Leu | |
| 125 | | | | | 130 | | | | | 135 | | | | | 140 | |
| ctg | aat | aac | ttc | tat | ccc | aga | gag | gcc | aaa | gta | cag | tg | aag | gtg | gat | 528 |
| Leu | Asn | Asn | Phe | Tyr | Pro | Arg | Glu | Ala | Lys | Val | Gln | Trp | Lys | Val | Asp | |
| | | | 145 | | | | | | 150 | | | | | 155 | | |
| aac | gcc | ctc | caa | tcg | gg | aac | tcc | cag | gag | agt | gtc | aca | gag | cag | gac | 576 |
| Asn | Ala | Leu | Gln | Ser | Gly | Asn | Ser | Gln | Glu | Ser | Val | Thr | Glu | Gln | Asp | |
| | | | 160 | | | | | 165 | | | | | 170 | | | |
| agc | aag | gac | agc | acc | tac | agc | ctc | agc | agc | acc | ctg | acg | ctg | agc | aaa | 624 |
| Ser | Lys | Asp | Ser | Thr | Tyr | Ser | Leu | Ser | Ser | Thr | Leu | Thr | Leu | Ser | Lys | |
| | | 175 | | | | | 180 | | | | | 185 | | | | |
| gca | gac | tac | gag | aaa | cac | aaa | gtc | tac | gcc | tgc | gaa | gtc | acc | cat | cag | 672 |
| Ala | Asp | Tyr | Glu | Lys | His | Lys | Val | Tyr | Ala | Cys | Glu | Val | Thr | His | Gln | |
| | 190 | | | | | 195 | | | | | 200 | | | | | |
| ggc | ctg | agc | tcg | ccc | gtc | aca | aag | agc | ttc | aac | agg | gga | gag | tgt | tag | 720 |
| Gly | Leu | Ser | Ser | Pro | Val | Thr | Lys | Ser | Phe | Asn | Arg | Gly | Glu | Cys | | |
| 205 | | | | | 210 | | | | 215 | | | | | | | |
| <210> 35 | | | | | | | | | | | | | | | | |
| <211> 239 | | | | | | | | | | | | | | | | |
| <212> PRT | | | | | | | | | | | | | | | | |
| <213> Homo sapiens | | | | | | | | | | | | | | | | |
| <400> 35 | | | | | | | | | | | | | | | | |
| Met | Arg | Phe | Ser | Ala | Gln | Leu | Leu | Gly | Leu | Leu | Val | Leu | Trp | Ile | Pro | |
| -20 | | | | | -15 | | | | | -10 | | | | | -5 | |
| Gly | Ser | Thr | Ala | Asp | Ile | Val | Met | Thr | Gln | Ser | Pro | Leu | Ser | Asn | Pro | |
| | | | -1 | 1 | | | | 5 | | | | | | 10 | | |
| Val | Thr | Leu | Gly | Glu | Ser | Gly | Ser | Ile | Ser | Cys | Arg | Ser | Ser | Lys | Ser | |
| | | 15 | | | | | 20 | | | | | 25 | | | | |
| Leu | Leu | His | Ser | Asn | Gly | Ile | Thr | Tyr | Leu | Tyr | Trp | Tyr | Leu | Gln | Lys | |
| | 30 | | | | | 35 | | | | | 40 | | | | | |
| Pro | Gly | Gln | Ser | Pro | Gln | Leu | Leu | Ile | Tyr | Gln | Met | Ser | Asn | Arg | Ala | |
| 45 | | | | | 50 | | | | | 55 | | | | | 60 | |
| Ser | Gly | Val | Pro | Asp | Arg | Phe | Ser | Ser | Ser | Gly | Ser | Gly | Thr | Asp | Phe | |
| | | | | 65 | | | | | 70 | | | | | 75 | | |

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
80 85 90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
95 100 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
110 115 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125 130 135 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145 150 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
160 165 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
175 180 185

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
190 195 200

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205 210 215

<210> 36
<211> 720
<212> DNA
<213> Homo sapiens

<220>
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<223> P2=P Human Engineered (low risk) ING1 light Chain with one
moderate risk proline change; proline at position 15 (P2)

<220>
<221> CDS
<222> (1)..(717)

<220>
<221> mat_peptide

<222> (61)..()

<400> 36

| | |
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| Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro | |
| -20 -15 -10 -5 | |
| gga tcc act gca gac atc gtg atg acc cag tct gca ctc tcc aat cca | 96 |
| Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro | |
| -1 1 5 10 | |
| gtc act cct gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt | 144 |
| Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser | |
| 15 20 25 | |
| ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa | 192 |
| Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys | |
| 30 35 40 | |
| cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc | 240 |
| Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala | |
| 45 50 55 60 | |
| tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc | 288 |
| Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe | |
| 65 70 75 | |
| act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac | 336 |
| Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr | |
| 80 85 90 | |
| tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag | 384 |
| Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys | |
| 95 100 105 | |
| ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg | 432 |
| Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro | |
| 110 115 120 | |
| cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg | 480 |
| Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu | |
| 125 130 135 140 | |
| ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat | 528 |
| Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp | |
| 145 150 155 | |
| aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac | 576 |
| Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp | |
| 160 165 170 | |
| agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa | 624 |
| Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys | |
| 175 180 185 | |

gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag 672
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
 190 195 200

ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag 720
 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 205 210 215

<210> 37
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 37

Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
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Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
 -1 1 5 10

Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
 15 20 25

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
 30 35 40

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
 45 50 55 60

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
 65 70 75

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 80 85 90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
 95 100 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
 110 115 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu

| | | | | | | |
|---|-----|-----|--|-----|--|-----|
| 125 | | 130 | | 135 | | 140 |
| Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp | | | | | | |
| | 145 | | | 150 | | 155 |
| Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp | | | | | | |
| | 160 | | | 165 | | 170 |
| Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys | | | | | | |
| | 175 | | | 180 | | 185 |
| Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln | | | | | | |
| | 190 | | | 195 | | 200 |
| Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys | | | | | | |
| | 205 | | | 210 | | 215 |

<210> 38
 <211> 720
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> P3=P Human Engineered (low risk) ING1 light Chain with one moderate risk proline change; proline at position 18 (P3)

<220>
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<220>
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 <222> (61)..()

| | |
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| Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro | |
| -20 -15 -10 -5 | |
| gga tcc act gca gac atc gtg atg acc cag tct gca ctc tcc aat cca | 96 |
| Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro | |
| -1 1 5 10 | |
| gtc act ctg gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt | 144 |
| Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser | |
| 15 20 25 | |

| | |
|---|-----|
| ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa | 192 |
| Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys | |
| 30 35 40 | |
| cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc | 240 |
| Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala | |
| 45 50 55 60 | |
| tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc | 288 |
| Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe | |
| 65 70 75 | |
| act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac | 336 |
| Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr | |
| 80 85 90 | |
| tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag | 384 |
| Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys | |
| 95 100 105 | |
| ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg | 432 |
| Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro | |
| 110 115 120 | |
| cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg | 480 |
| Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu | |
| 125 130 135 140 | |
| ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat | 528 |
| Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp | |
| 145 150 155 | |
| aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac | 576 |
| Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp | |
| 160 165 170 | |
| agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa | 624 |
| Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys | |
| 175 180 185 | |
| gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag | 672 |
| Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln | |
| 190 195 200 | |
| ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag | 720 |
| Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys | |
| 205 210 215 | |

<210> 39
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 39

Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20 -15 -10 -5

Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
-1 1 5 10

Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
15 20 25

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
30 35 40

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45 50 55 60

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
65 70 75

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
80 85 90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
95 100 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
110 115 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125 130 135 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145 150 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
160 165 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
175 180 185

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
190 195 200

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205 210 215

<210> 40
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> P1P2=Human Engineered (low risk) ING1 light Chain with one
moderate risk proline change; proline at position 8 (P1) 15(P2)

<220>
<221> CDS
<222> (1)..(717)

<220>
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<222> (61)..()

<400> 40
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Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20 -15 -10 -5

gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca 96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
-1 1 5 10

gtc act cct gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt 144
Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
15 20 25

ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa 192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
30 35 40

cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc 240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45 50 55 60

tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc 288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
65 70 75

act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac 336

| | | | | | | | | | | | | | | | | | |
|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Leu | Lys | Ile | Ser | Arg | Val | Glu | Ala | Glu | Asp | Val | Gly | Val | Tyr | Tyr | | |
| | | | 80 | | | | | 85 | | | | | 90 | | | | |
| tgt | gct | cag | aac | cta | gag | ctt | ccg | cgg | acg | ttc | ggg | cag | ggc | acc | aag | 384 | |
| Cys | Ala | Gln | Asn | Leu | Glu | Leu | Pro | Arg | Thr | Phe | Gly | Gln | Gly | Thr | Lys | | |
| | | 95 | | | | | 100 | | | | | 105 | | | | | |
| ctt | gag | atg | aaa | cga | act | gtg | gct | gca | cca | tct | gtc | ttc | atc | ttc | ccg | 432 | |
| Leu | Glu | Met | Lys | Arg | Thr | Val | Ala | Ala | Pro | Ser | Val | Phe | Ile | Phe | Pro | | |
| | 110 | | | | | 115 | | | | | 120 | | | | | | |
| cca | tct | gat | gag | cag | ttg | aaa | tct | gga | act | gcc | tct | gtt | gtg | tgc | ctg | 480 | |
| Pro | Ser | Asp | Glu | Gln | Leu | Lys | Ser | Gly | Thr | Ala | Ser | Val | Val | Cys | Leu | | |
| 125 | | | | | 130 | | | | | 135 | | | | | 140 | | |
| ctg | aat | aac | ttc | tat | ccc | aga | gag | gcc | aaa | gta | cag | tgg | aag | gtg | gat | 528 | |
| Leu | Asn | Asn | Phe | Tyr | Pro | Arg | Glu | Ala | Lys | Val | Gln | Trp | Lys | Val | Asp | | |
| | | | | 145 | | | | | 150 | | | | | 155 | | | |
| aac | gcc | ctc | caa | tcg | ggg | aac | tcc | cag | gag | agt | gtc | aca | gag | cag | gac | 576 | |
| Asn | Ala | Leu | Gln | Ser | Gly | Asn | Ser | Gln | Glu | Ser | Val | Thr | Glu | Gln | Asp | | |
| | | | 160 | | | | | 165 | | | | | 170 | | | | |
| agc | aag | gac | agc | acc | tac | agc | ctc | agc | agc | acc | ctg | acg | ctg | agc | aaa | 624 | |
| Ser | Lys | Asp | Ser | Thr | Tyr | Ser | Leu | Ser | Ser | Thr | Leu | Thr | Leu | Ser | Lys | | |
| | | 175 | | | | | 180 | | | | | 185 | | | | | |
| gca | gac | tac | gag | aaa | cac | aaa | gtc | tac | gcc | tgc | gaa | gtc | acc | cat | cag | 672 | |
| Ala | Asp | Tyr | Glu | Lys | His | Lys | Val | Tyr | Ala | Cys | Glu | Val | Thr | His | Gln | | |
| | 190 | | | | | 195 | | | | | 200 | | | | | | |
| ggc | ctg | agc | tcg | ccc | gtc | aca | aag | agc | ttc | aac | agg | gga | gag | tgt | tag | 720 | |
| Gly | Leu | Ser | Ser | Pro | Val | Thr | Lys | Ser | Phe | Asn | Arg | Gly | Glu | Cys | | | |
| 205 | | | | | 210 | | | | 215 | | | | | | | | |
| <210> 41 | | | | | | | | | | | | | | | | | |
| <211> 239 | | | | | | | | | | | | | | | | | |
| <212> PRT | | | | | | | | | | | | | | | | | |
| <213> Homo sapiens | | | | | | | | | | | | | | | | | |
| <400> 41 | | | | | | | | | | | | | | | | | |
| Met | Arg | Phe | Ser | Ala | Gln | Leu | Leu | Gly | Leu | Leu | Val | Leu | Trp | Ile | Pro | | |
| -20 | | | | | -15 | | | | | -10 | | | | | -5 | | |
| Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro | | | | | | | | | | | | | | | | | |
| | | | -1 | 1 | | | | 5 | | | | | 10 | | | | |
| Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser | | | | | | | | | | | | | | | | | |
| | | 15 | | | | | 20 | | | | | 25 | | | | | |

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
30 35 40

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45 50 55 60

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
65 70 75

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
80 85 90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
95 100 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
110 115 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125 130 135 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145 150 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
160 165 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
175 180 185

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
190 195 200

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205 210 215

<210> 42

<211> 720

<212> DNA

<213> Homo sapiens

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<220>
<221> misc_feature
<223> P1P3= Human Engineered (low risk) ING1 light Chain with one
      moderate risk proline change; proline at position 8 (P1) 18 (P3)

<220>
<221> CDS
<222> (1)..(717)

<220>
<221> mat_peptide
<222> (61)..()

<400> 42
atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct      48
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20                      -15                      -10                      -5

gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca      96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
      -1  1                      5                      10

gtc act ctg gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt     144
Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
      15                      20                      25

ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa     192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
      30                      35                      40

cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc     240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45                      50                      55                      60

tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc     288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
      65                      70                      75

act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac     336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
      80                      85                      90

tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag     384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
      95                      100                      105

ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg     432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
      110                      115                      120

cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg     480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125                      130                      135                      140

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ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat 528
 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
 145 150 155

aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac 576
 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 160 165 170

agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa 624
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 175 180 185

gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag 672
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
 190 195 200

ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag 720
 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 205 210 215

<210> 43
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 43

Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
 -20 -15 -10 -5

Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
 -1 1 5 10

Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
 15 20 25

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
 30 35 40

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
 45 50 55 60

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
 65 70 75

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 80 | | 85 | | 90 | | | | | | | | | | |
| Cys | Ala | Gln | Asn | Leu | Glu | Leu | Pro | Arg | Thr | Phe | Gly | Gln | Gly | Thr | Lys |
| | 95 | | | | | | 100 | | | | | 105 | | | |
| Leu | Glu | Met | Lys | Arg | Thr | Val | Ala | Ala | Pro | Ser | Val | Phe | Ile | Phe | Pro |
| 110 | | | | | | 115 | | | | | 120 | | | | |
| Pro | Ser | Asp | Glu | Gln | Leu | Lys | Ser | Gly | Thr | Ala | Ser | Val | Val | Cys | Leu |
| 125 | | | | | 130 | | | | | 135 | | | | | 140 |
| Leu | Asn | Asn | Phe | Tyr | Pro | Arg | Glu | Ala | Lys | Val | Gln | Trp | Lys | Val | Asp |
| | | | 145 | | | | | | 150 | | | | | 155 | |
| Asn | Ala | Leu | Gln | Ser | Gly | Asn | Ser | Gln | Glu | Ser | Val | Thr | Glu | Gln | Asp |
| | | 160 | | | | | | 165 | | | | | | 170 | |
| Ser | Lys | Asp | Ser | Thr | Tyr | Ser | Leu | Ser | Ser | Thr | Leu | Thr | Leu | Ser | Lys |
| | | 175 | | | | | 180 | | | | | 185 | | | |
| Ala | Asp | Tyr | Glu | Lys | His | Lys | Val | Tyr | Ala | Cys | Glu | Val | Thr | His | Gln |
| 190 | | | | | | 195 | | | | | 200 | | | | |
| Gly | Leu | Ser | Ser | Pro | Val | Thr | Lys | Ser | Phe | Asn | Arg | Gly | Glu | Cys | |
| 205 | | | | | 210 | | | | | 215 | | | | | |

<210> 44

<211> 720

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> P2P3=Human Engineered (low risk) ING1 light Chain with one moderate risk proline change; proline at position 8 (P1) 18 (P3)

<220>

<221> CDS

<222> (1)..(717)

<220>

<221> mat_peptide

<222> (61)..()

| | | | | | | | | | | | | | | | | |
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| <400> | 44 | | | | | | | | | | | | | | | |
| atg | agg | ttc | tct | gct | cag | ctt | ctg | ggg | ctg | ctt | gtg | ctc | tgg | atc | cct | 48 |
| Met | Arg | Phe | Ser | Ala | Gln | Leu | Leu | Gly | Leu | Leu | Val | Leu | Trp | Ile | Pro | |
| | | | | | -15 | | | | | | -10 | | | | | |
| gga | tcc | act | gca | gac | atc | gtg | atg | acc | cag | tct | gca | ctc | tcc | aat | cca | 96 |
| Gly | Ser | Thr | Ala | Asp | Ile | Val | Met | Thr | Gln | Ser | Ala | Leu | Ser | Asn | Pro | |
| | | | -1 | 1 | | | | 5 | | | | 10 | | | | |
| gtc | act | cct | gga | gag | ccg | ggt | tcc | atc | tcc | tgc | cgg | tct | agt | aag | agt | 144 |
| Val | Thr | Pro | Gly | Glu | Pro | Gly | Ser | Ile | Ser | Cys | Arg | Ser | Ser | Lys | Ser | |
| | | 15 | | | | 20 | | | | 25 | | | | | | |
| ctc | cta | cat | agt | aat | ggc | atc | act | tat | ttg | tat | tgg | tat | ctg | cag | aaa | 192 |
| Leu | Leu | His | Ser | Asn | Gly | Ile | Thr | Tyr | Leu | Tyr | Trp | Tyr | Leu | Gln | Lys | |
| | | 30 | | | | 35 | | | | 40 | | | | | | |
| cca | ggg | cag | tct | cct | cag | ctg | ctc | atc | tat | cag | atg | tct | aac | aga | gcc | 240 |
| Pro | Gly | Gln | Ser | Pro | Gln | Leu | Leu | Ile | Tyr | Gln | Met | Ser | Asn | Arg | Ala | |
| 45 | | | | | 50 | | | | 55 | | | | | | 60 | |
| tca | ggg | gtc | cca | gac | agg | ttc | agt | agc | agt | gga | tct | ggg | aca | gat | ttc | 288 |
| Ser | Gly | Val | Pro | Asp | Arg | Phe | Ser | Ser | Ser | Gly | Ser | Gly | Thr | Asp | Phe | |
| | | | | 65 | | | | 70 | | | | 75 | | | | |
| act | ctc | aag | atc | agc | aga | gtg | gag | gct | gaa | gat | gtg | gga | gtt | tat | tac | 336 |
| Thr | Leu | Lys | Ile | Ser | Arg | Val | Glu | Ala | Glu | Asp | Val | Gly | Val | Tyr | Tyr | |
| | | | 80 | | | | 85 | | | | 90 | | | | | |
| tgt | gct | cag | aac | cta | gag | ctt | ccg | cgg | acg | ttc | ggt | cag | ggc | acc | aag | 384 |
| Cys | Ala | Gln | Asn | Leu | Glu | Leu | Pro | Arg | Thr | Phe | Gly | Gln | Gly | Thr | Lys | |
| | | 95 | | | | 100 | | | | 105 | | | | | | |
| ctt | gag | atg | aaa | cga | act | gtg | gct | gca | cca | tct | gtc | ttc | atc | ttc | ccg | 432 |
| Leu | Glu | Met | Lys | Arg | Thr | Val | Ala | Ala | Pro | Ser | Val | Phe | Ile | Phe | Pro | |
| | | 110 | | | | 115 | | | | 120 | | | | | | |
| cca | tct | gat | gag | cag | ttg | aaa | tct | gga | act | gcc | tct | gtt | gtg | tgc | ctg | 480 |
| Pro | Ser | Asp | Glu | Gln | Leu | Lys | Ser | Gly | Thr | Ala | Ser | Val | Val | Cys | Leu | |
| 125 | | | | | 130 | | | | 135 | | | | | | 140 | |
| ctg | aat | aac | ttc | tat | ccc | aga | gag | gcc | aaa | gta | cag | tgg | aag | gtg | gat | 528 |
| Leu | Asn | Asn | Phe | Tyr | Pro | Arg | Glu | Ala | Lys | Val | Gln | Trp | Lys | Val | Asp | |
| | | | 145 | | | | 150 | | | | 155 | | | | | |
| aac | gcc | ctc | caa | tcg | ggt | aac | tcc | cag | gag | agt | gtc | aca | gag | cag | gac | 576 |
| Asn | Ala | Leu | Gln | Ser | Gly | Asn | Ser | Gln | Glu | Ser | Val | Thr | Glu | Gln | Asp | |
| | | | 160 | | | | 165 | | | | 170 | | | | | |
| agc | aag | gac | agc | acc | tac | agc | ctc | agc | agc | acc | ctg | acg | ctg | agc | aaa | 624 |
| Ser | Lys | Asp | Ser | Thr | Tyr | Ser | Leu | Ser | Ser | Thr | Leu | Thr | Leu | Ser | Lys | |
| | | 175 | | | | 180 | | | | 185 | | | | | | |
| gca | gac | tac | gag | aaa | cac | aaa | gtc | tac | gcc | tgc | gaa | gtc | acc | cat | cag | 672 |

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
190 195 200

ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag 720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205 210 215

<210> 45
<211> 239
<212> PRT
<213> Homo sapiens

<400> 45

Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20 -15 -10 -5

Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
-1 1 5 10

Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
15 20 25

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
30 35 40

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45 50 55 60

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
65 70 75

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
80 85 90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
95 100 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
110 115 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125 130 135 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145 150 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
160 165 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
175 180 185

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
190 195 200

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205 210 215

<210> 46
<211> 85
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> P1 Oligo Human Engineered ING-1 with proline oligos

<400> 46
actcttacta gaccggcagg agatggaacc tgactctccc agagtgactg gattggagag 60
tggagactgg gtcacacga tgtct 85

<210> 47
<211> 85
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> P2 Oligo Human Engineered ING-1 with proline oligos

<400> 47
actcttacta gaccggcagg agatggaacc tgactctcca ggagtgactg gattggagag 60
tgcagactgg gtcacacga tgtct 85

<210> 48

<211> 85
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> P3 Oligo Human Engineered ING-1 with proline oligos

<400> 48
actcttacta gaccggcagg agatggaacc cggctctccc agagtgactg gattggagag 60
tgcagactgg gtcatcacga tgtct 85

<210> 49
<211> 85
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> P1P2 Oligo Human Engineered ING-1 with proline oligos

<400> 49
actcttacta gaccggcagg agatggaacc cggctctcca ggagtgactg gattggagag 60
tgcagactgg gtcatcacga tgtct 85

<210> 50
<211> 85
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> P1P3 Oligo Human Engineered ING-1 with proline oligos

<400> 50
actcttacta gaccggcagg agatggaacc cggctctccc agagtgactg gattggagag 60
tggagactgg gtcatcacga tgtct 85

<210> 51
<211> 85
<212> DNA
<213> Homo Sapiens

<220>


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<221> misc_feature
<223> P2P3 Oligo Human Engineered ING-1 with proline oligos

<400> 51
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tgcagactgg gtcattcacga tgtct                                           85

<210> 52
<211> 19
<212> DNA
<213> Homo Sapiens

<220>
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<223> Reverse Primer KBsr ING-1 Light Chain

<400> 52
cttactagac cggcaggag                                                    19

<210> 53
<211> 798
<212> DNA
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<220>
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<223> EpCam truncated sequence

<220>
<221> CDS
<222> (1)..(795)

<400> 53
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Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
1          5          10          15

acg gcg act ttt gcc gca gct cag gaa gaa tgt gtc tgt gaa aac tac      96
Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
          20          25          30

aag ctg gcc gta aac tgc ttt gtg aat aat aat cgt caa tgc cag tgt      144
Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
          35          40          45

act tca gtt ggt gca caa aat act gtc att tgc tca aag ctg gct gcc      192
Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
          50          55          60

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| | |
|---|-----|
| aaa tgt ttg gtg atg aag gca gaa atg aat ggc tca aaa ctt ggg aga | 240 |
| Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg | |
| 65 70 75 80 | |
| aga gca aaa cct gaa ggg gcc ctc cag aac aat gat ggg ctt tat gat | 288 |
| Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asp Gly Leu Tyr Asp | |
| 85 90 95 | |
| cct gac tgc gat gag agc ggg ctc ttt aag gcc aag cag tgc aac ggc | 336 |
| Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly | |
| 100 105 110 | |
| acc tcc acg tgc tgg tgt gtg aac act gct ggg gtc aga aga aca gac | 384 |
| Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp | |
| 115 120 125 | |
| aag gac act gaa ata acc tgc tct gag cga gtg aga acc tac tgg atc | 432 |
| Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile | |
| 130 135 140 | |
| atc att gaa cta aaa cac aaa gca aga gaa aaa cct tat gat agt aaa | 480 |
| Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys | |
| 145 150 155 160 | |
| agt ttg cgg act gca ctt cag aag gag atc aca acg cgt tat caa ctg | 528 |
| Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu | |
| 165 170 175 | |
| gat cca aaa ttt atc acg agt att ttg tat gag aat aat gtt atc act | 576 |
| Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr | |
| 180 185 190 | |
| att gat ctg gtt caa aat tct tct caa aaa act cag aat gat gtg gac | 624 |
| Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp | |
| 195 200 205 | |
| ata gct gat gtg gct tat tat ttt gaa aaa gat gtt aaa ggt gaa tcc | 672 |
| Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser | |
| 210 215 220 | |
| ttg ttt cat tct aag aaa atg gac ctg aca gta aat ggg gaa caa ctg | 720 |
| Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu | |
| 225 230 235 240 | |
| gat ctg gat cct ggt caa act tta att tat tat gtt gat gaa aaa gca | 768 |
| Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala | |
| 245 250 255 | |
| cct gaa ttc tca atg cag ggt cta aaa taa | 798 |
| Pro Glu Phe Ser Met Gln Gly Leu Lys | |
| 260 265 | |

<211> 265
<212> PRT
<213> Homo sapiens

<400> 54

Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
1 5 10 15

Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
20 25 30

Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
35 40 45

Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
50 55 60

Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
65 70 75 80

Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
85 90 95

Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
100 105 110

Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
115 120 125

Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
130 135 140

Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
145 150 155 160

Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
165 170 175

Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
180 185 190

Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
 195 200 205

Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
 210 215 220

Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
 225 230 235 240

Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
 245 250 255

Pro Glu Phe Ser Met Gln Gly Leu Lys
 260 265

<210> 55
 <211> 945
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Full-Length EpCam

<220>
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<220>
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 <222> (70)..()

<400> 55
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 Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
 -20 -15 -10

acg gcg act ttt gcc gca gct cag gaa gaa tgt gtc tgt gaa aac tac 96
 Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
 -5 -1 1 5

aag ctg gcc gta aac tgc ttt gtg aat aat aat cgt caa tgc cag tgt 144
 Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
 10 15 20 25

act tca gtt ggt gca caa aat act gtc att tgc tca aag ctg gct gcc 192
 Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
 30 35 40

| | |
|---|-----|
| aaa tgt ttg gtg atg aag gca gaa atg aat ggc tca aaa ctt ggg aga | 240 |
| Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg | |
| 45 50 55 | |
| aga gca aaa cct gaa ggg gcc ctc cag aac aat gat ggg ctt tat gat | 288 |
| Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp | |
| 60 65 70 | |
| cct gac tgc gat gag agc ggg ctc ttt aag gcc aag cag tgc aac ggc | 336 |
| Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly | |
| 75 80 85 | |
| acc tcc acg tgc tgg tgt gtg aac act gct ggg gtc aga aga aca gac | 384 |
| Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp | |
| 90 95 100 105 | |
| aag gac act gaa ata acc tgc tct gag cga gtg aga acc tac tgg atc | 432 |
| Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile | |
| 110 115 120 | |
| atc att gaa cta aaa cac aaa gca aga gaa aaa cct tat gat agt aaa | 480 |
| Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys | |
| 125 130 135 | |
| agt ttg cgg act gca ctt cag aag gag atc aca acg cgt tat caa ctg | 528 |
| Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu | |
| 140 145 150 | |
| gat cca aaa ttt atc acg agt att ttg tat gag aat aat gtt atc act | 576 |
| Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr | |
| 155 160 165 | |
| att gat ctg gtt caa aat tct tct caa aaa act cag aat gat gtg gac | 624 |
| Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp | |
| 170 175 180 185 | |
| ata gct gat gtg gct tat tat ttt gaa aaa gat gtt aaa ggt gaa tcc | 672 |
| Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser | |
| 190 195 200 | |
| ttg ttt cat tct aag aaa atg gac ctg aca gta aat ggg gaa caa ctg | 720 |
| Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu | |
| 205 210 215 | |
| gat ctg gat cct ggt caa act tta att tat tat gtt gat gaa aaa gca | 768 |
| Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala | |
| 220 225 230 | |
| cct gaa ttc tca atg cag ggt cta aaa gct ggt gtt att gct gtt att | 816 |
| Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile | |
| 235 240 245 | |
| gtg gtt gtg gtg ata gca gtt gtt gct gga att gtt gtg ctg gtt att | 864 |

Val Val Val Val Ile Ala Val Val Ala Gly Ile Val Val Leu Val Ile
250 255 260 265

tcc aga aag aag aga atg gca aag tat gag aag gct gag ata aag gag 912
Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
270 275 280

atg ggt gag atg cat agg gaa ctc aat gca taa 945
Met Gly Glu Met His Arg Glu Leu Asn Ala
285 290

<210> 56

<211> 314

<212> PRT

<213> Homo sapiens

<400> 56

Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
-20 -15 -10

Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
-5 -1 1 5

Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
10 15 20 25

Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
30 35 40

Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
45 50 55

Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
60 65 70

Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
75 80 85

Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
90 95 100 105

Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
110 115 120

Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
125 130 135

Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
140 145 150

Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
155 160 165

Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
170 175 180 185

Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
190 195 200

Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
205 210 215

Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
220 225 230

Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
235 240 245

Val Val Val Val Ile Ala Val Val Ala Gly Ile Val Val Leu Val Ile
250 255 260 265

Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
270 275 280

Met Gly Glu Met His Arg Glu Leu Asn Ala
285 290

<210> 57
<211> 26
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Forward Primer (for both soluble and full length Ep-CAM): EC-1

<400> 57
ttatgtcgac agcatggcgc ccccgc 26

<210> 58
<211> 31
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Ep-CAM Reverse Primer (for soluble Ep-CAM): EC-2

<400> 58
gagttacgtc ccagatttta ttgggcccc t 31

<210> 59
<211> 30
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Ep-CAM Reverse Primer (for full-length Ep-CAM): EC-3

<400> 59
gtatcccttg agttacgtat tgagctcgtt 30